

## SEQUENCE LISTING

<110> WOLF, SABINE  
 JAGER, MARTINA  
 BANGSOW, THORSTEN  
 BANGSOW, CARMEN  
 JORDAN, DOMINIK  
 PELZER, BERNHARD  
 OPPOLZER, THOMAS

<120> METHOD FOR IDENTIFYING BBB-SPECIFIC PROTEINS AND  
 FRAGMENTS THEREOF

<130> 63047(45107)

<140> 10/527,788

<141> 2005-03-11

<150> PCT/EP03/09968

<151> 2003-03-08

<150> DE 102 42 016.5

<151> 2002-09-11

<160> 70

<170> PatentIn Ver. 3.3

<210> 1

<211> 323

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<223> Description of Artificial Sequence: Synthetic  
 clone S129 from BMEC from swine brain

<400> 1

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tggaggccct cgtaagccat acgggtccgtg ctcagatcct gactggcaag gaactccaag 180
ttgccactaa ggaaaaagag ggcttctctg ggagatgcat gcttactctc gtaggccttt 240
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<210> 2

<211> 22

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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acctccattg ttatgcctcc ta
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<210> 3  
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 primer

<400> 3  
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<220>  
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 <222> (119)..(910)

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 <223> a, c, g, t, unknown, or other

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 tgcagccgag gacaacactg attcgagccg tgacctaccg gccgcgggaa ttcgattt 118  
 atg gtg aaa atc gcc ttc aat aca ccc gca gcg gtg caa aaa gag gag 166  
 Met Val Lys Ile Ala Phe Asn Thr Pro Ala Ala Val Gln Lys Glu Glu  
 1 5 10 15  
 gcg cag caa gac gtg gag gcc ctc gta agc cat acg gtc cgt gct cag 214  
 Ala Gln Gln Asp Val Glu Ala Leu Val Ser His Thr Val Arg Ala Gln  
 20 25 30  
 atc ctg act ggc aag gaa ctc caa gtt gcc act aag gaa aaa gag ggc 262  
 Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly  
 35 40 45  
 ttc tct ggg aga tgc atg ctt act ctc gta ggc ctt tcc ttc atc ttg 310  
 Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu  
 50 55 60  
 gca gga ctt att gtt ggt gga gcc tgc att tac aag tac ttc atg ccc 358  
 Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro  
 65 70 75 80  
 aag agt acc atc tac cat gga gag atg tgc ttc ttt gat tct gcg gac 406  
 Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp  
 85 90 95

cct gca aat ttc ctc caa gga gga gag ccc tac ttc ctg cct gtg atg 454  
 Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met  
 100 105 110

gaa gag gct gat att cgt gaa gat gac aac att gca atc att gat gtg 502  
 Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val  
 115 120 125

cct gtc ccc agt ttc tct gat agt gac cct gca gca att att cat gac 550  
 Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp  
 130 135 140

ttt gaa aag ggc atg act gct tac ctg gac ttg ctg ctg ggg aac tgc 598  
 Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys  
 145 150 155 160

tat ctg atg ccc ctc aat acc tcc att gtt atg cct cct aag tat ctc 646  
 Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu  
 165 170 175

gtg gag ctc ttt ggc aaa ctg gca cgt ggc aaa tac ctc cct cac gct 694  
 Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala  
 180 185 190

tat gtg gtt cat gaa gac ctg gtt gct gtg gaa gag att cat gat gtt 742  
 Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val  
 195 200 205

agt aac ctt ggc atc ttt att tac caa ctt tgc aac aac cgc aag tct 790  
 Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser  
 210 215 220

ttc cgc ctt cgt aga aga gac ctc ttg ctg ggt ttc aac aaa cgt gcc 838  
 Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala  
 225 230 235 240

att gat aag tgc tgg aag att aga cac ttc ccc aat gaa ttt att gtt 886  
 Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val  
 245 250 255

gag acc aag atc tgt caa gag tga gaggcaacag aaaaagagtg tacttagtaa 940  
 Glu Thr Lys Ile Cys Gln Glu  
 260

taggaagtca aagatttaca atatgacttc aatattaaag tgtgtaggac attcaagata 1000

ttactcatg catttcctct attgcttata cttaaaaaaa agaaagaaaa taaaaactac 1060

taaccattgc aaaaaaaaaa aaaaaaagta ctagtgcacg cgtggccaga aactgaaatg 1120

aatgattttt tatgtttttc cttttgaatt tatagggttt atgttttntt gaatgcaatg 1180

tgaaggtgtt ggctaacatc ctgacaatga attccatccc ttgtgtatat gtgtgtcttt 1240

aaaagtaaaa tyttcartca tatggtaaaa catgttttaa atttaaaata tttaaaattg 1300

ttttcaacct ttttgtgtag cgcttgtcaa atatcttaac attgtcttgt tttgttttca 1360

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<212> PRT  
<213> Sus sp.

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Ile Leu Thr Gly Lys Glu Leu Gln Val Ala Thr Lys Glu Lys Glu Gly  
35 40 45  
Phe Ser Gly Arg Cys Met Leu Thr Leu Val Gly Leu Ser Phe Ile Leu  
50 55 60  
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro  
65 70 75 80  
Lys Ser Thr Ile Tyr His Gly Glu Met Cys Phe Phe Asp Ser Ala Asp  
85 90 95  
Pro Ala Asn Phe Leu Gln Gly Gly Glu Pro Tyr Phe Leu Pro Val Met  
100 105 110  
Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val  
115 120 125  
Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp  
130 135 140  
Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys  
145 150 155 160  
Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Tyr Leu  
165 170 175  
Val Glu Leu Phe Gly Lys Leu Ala Arg Gly Lys Tyr Leu Pro His Ala  
180 185 190  
Tyr Val Val His Glu Asp Leu Val Ala Val Glu Glu Ile His Asp Val  
195 200 205  
Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser  
210 215 220

Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala  
 225 230 235 240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val  
 245 250 255

Glu Thr Lys Ile Cys Gln Glu  
 260

<210> 6  
 <211> 814  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 clone S231 from BMEC from swine brain

<220>  
 <221> modified\_base  
 <222> (712)  
 <223> a, c, g, t, unknown, or other

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 atttaatgat cacatgagta tagaaagctg ttttgagtgc tgaaacagac ttacctatca 180  
 gatatatcca aaagagattc tatgttaaaa agtcagacta tgactggagt gaaccatgta 240  
 ttcccttgct ttttactttg tttctgtgac atttatgttt catgtaactt gcattatggg 300  
 tgggtgggtt gtcctagtagt tgtatttttg cttcttcttt aataggattg atatttcata 360  
 tabtataatt gtgaatattt tgakacraat gtttataact ctaggcatat aaaaacagat 420  
 tctgattccc ttcactgtgt gaatgttttc tgttgaaaaa atggaggata aatatggata 480  
 ctaatgacac tcattcctaa ttaagttttc aatcagtttg atttgataa cttgcattta 540  
 tccgagatat tgagctactt tctgataatg catcaagcat ttctaccata actctttcac 600  
 gcaactgaat gttgttaagt atagttttat cttgctttaa ttaaacttct taagcaaaaa 660  
 aaaagaaact tcataagcta atacattaga gaaagggttat gatcttgaat cnagaatggc 720  
 ttatggcatt aaggaatgag atacttgtaa attttctttg aaacagccaa ctctctgtgt 780  
 gtgtcttcac aattcaaaag atatgcctca ctgt 814

<210> 7  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 7  
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<210> 8  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 8  
acaacagagg agttggctgt tt 22

<210> 9  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 9  
ggtattgctg gctggatatct tt 22

<210> 10  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 10  
atgtaggaat agccgtggtg at 22

<210> 11  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 11  
ggtctttgtg ttccagctct tc 22

<210> 12  
<211> 23  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

&lt;400&gt; 12

ttctcaggac cagatagaga acg

23

&lt;210&gt; 13

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic clone S231 from BMEC from swine brain

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(480)

&lt;400&gt; 13

atg	ttg	gtg	tta	ctg	gct	ggg	atc	ttt	gtg	gtc	cac	atc	gcc	act	gtc	48
Met	Leu	Val	Leu	Leu	Ala	Gly	Ile	Phe	Val	Val	His	Ile	Ala	Thr	Val	
1				5					10					15		

gtc	atg	ctg	ttc	gtt	tgc	acc	att	gcc	aat	gtc	tgg	gtg	gtc	tca	gat	96
Val	Met	Leu	Phe	Val	Cys	Thr	Ile	Ala	Asn	Val	Trp	Val	Val	Ser	Asp	
		20						25					30			

gcg	gga	caa	gga	tct	gtc	ggg	ctt	tgg	aaa	aac	tgt	acc	agt	gct	ggc	144
Ala	Gly	Gln	Gly	Ser	Val	Gly	Leu	Trp	Lys	Asn	Cys	Thr	Ser	Ala	Gly	
		35					40					45				

tgt	act	gat	acc	ctg	tta	tac	ggc	ggg	gaa	gat	gcc	ctc	aag	tcg	gtg	192
Cys	Thr	Asp	Thr	Leu	Leu	Tyr	Gly	Gly	Glu	Asp	Ala	Leu	Lys	Ser	Val	
	50					55					60					

cag	gcc	ttc	atg	atc	ctg	tct	atc	atc	ttc	tct	gtc	gtc	tcc	ctc	gtg	240
Gln	Ala	Phe	Met	Ile	Leu	Ser	Ile	Ile	Phe	Ser	Val	Val	Ser	Leu	Val	
65					70				75					80		

gtc	ttt	gtg	ttc	cag	ctc	ttc	acc	atg	gag	aaa	ggc	aac	cgc	ttc	ttc	288
Val	Phe	Val	Phe	Gln	Leu	Phe	Thr	Met	Glu	Lys	Gly	Asn	Arg	Phe	Phe	
				85					90					95		

ctc	tcg	gga	gcc	acc	atg	ctg	gtg	tgc	tgg	ctg	tgc	atc	atg	gtg	ggg	336
Leu	Ser	Gly	Ala	Thr	Met	Leu	Val	Cys	Trp	Leu	Cys	Ile	Met	Val	Gly	
			100					105					110			

gcc	tcc	gtc	tat	act	cat	cat	tat	gcc	aac	agt	tct	aaa	aac	caa	tac	384
Ala	Ser	Val	Tyr	Thr	His	His	Tyr	Ala	Asn	Ser	Ser	Lys	Asn	Gln	Tyr	
		115					120					125				

tcg	gcg	agt	cac	cat	ggc	tat	tcc	ttc	atc	ctc	gcc	tgg	atc	tgc	ttc	432
Ser	Ala	Ser	His	His	Gly	Tyr	Ser	Phe	Ile	Leu	Ala	Trp	Ile	Cys	Phe	
	130					135					140					

tgc ttc agc ttc atc atc ggc gtt ctc tat ctg gtc ctg aga aag aaa 480  
 Cys Phe Ser Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys  
 145 150 155 160

taa 483

<210> 14

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 clone S231 from BMEC from swine brain

<400> 14

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 1 5 10 15

Val Met Leu Phe Val Cys Thr Ile Ala Asn Val Trp Val Val Ser Asp  
 20 25 30

Ala Gly Gln Gly Ser Val Gly Leu Trp Lys Asn Cys Thr Ser Ala Gly  
 35 40 45

Cys Thr Asp Thr Leu Leu Tyr Gly Gly Glu Asp Ala Leu Lys Ser Val  
 50 55 60

Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Ser Val Val Ser Leu Val  
 65 70 75 80

Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe  
 85 90 95

Leu Ser Gly Ala Thr Met Leu Val Cys Trp Leu Cys Ile Met Val Gly  
 100 105 110

Ala Ser Val Tyr Thr His His Tyr Ala Asn Ser Ser Lys Asn Gln Tyr  
 115 120 125

Ser Ala Ser His His Gly Tyr Ser Phe Ile Leu Ala Trp Ile Cys Phe  
 130 135 140

Cys Phe Ser Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys  
 145 150 155 160

<210> 15

<211> 513

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 clone S012 from BMEC from swine brain

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taaatttaac cttttaatta tcacctcacc tgaaaagggt gggtgagata ctacgcagc 180
atgtattata ttaaccatgt catgtttaag ttattaaatt cagattattt ataacttatt 240
atcttagggc ctgcctcatg tcttctaggg tatttgagta atcatcctat atttaaagtt 300
aaaactttga cttaaaaaac actgttaatg aaagttccct agcgcttttc ttattttcaa 360
attggtctta tgggtagtag tagagaattc catgctgttc tgaggctagc ttccaggtaa 420
acagtgattt ttttttctt tttttcttc tttcttggtg agtgggtccag agttttaagc 480
tacttttctc aaagtttcaa ccctttccca ggt 513

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<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
        primer

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<400> 16
gtatcgggag tggaggatta ca 22

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<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
        primer

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<400> 17
cccgaggtat atttgtttct gg 22

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<210> 18
<211> 1674
<212> DNA
<213> Sus sp.

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<220>
<221> CDS
<222> (40)..(774)

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                                   Met Phe Val Ala Ala
                                   1           5

cgg aca ggc cag aga acc ttg aga aag gtg gtc tgc gga tgc cgt cca 102
Arg Thr Gly Gln Arg Thr Leu Arg Lys Val Ser Gly Cys Arg Pro
      10                15                20

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aaa tcg gcg aca gcg act gga gtc ccg gct cct gcg cag ggg cct ccg	150
Lys Ser Ala Thr Ala Thr Gly Val Pro Ala Pro Ala Gln Gly Pro Pro	
25 30 35	
cgg aac atc aga tac tta gcc tcc tgt ggt ata ctg atg aac aga act	198
Arg Asn Ile Arg Tyr Leu Ala Ser Cys Gly Ile Leu Met Asn Arg Thr	
40 45 50	
ctt cca ctg cat tcc tca ttt ttg cct aag gag atg tat gca aga acc	246
Leu Pro Leu His Ser Ser Phe Leu Pro Lys Glu Met Tyr Ala Arg Thr	
55 60 65	
ttc ttc aga att gct gca cca tta ata aac aaa aga aaa gaa tat tca	294
Phe Phe Arg Ile Ala Ala Pro Leu Ile Asn Lys Arg Lys Glu Tyr Ser	
70 75 80 85	
gag agg agg att ata gga tat tct atg cag gaa atg tat gac gta gta	342
Glu Arg Arg Ile Ile Gly Tyr Ser Met Gln Glu Met Tyr Asp Val Val	
90 95 100	
tcg gga atg gaa gat tac aag cat ttt gtg cct tgg tgc aaa aaa tca	390
Ser Gly Met Glu Asp Tyr Lys His Phe Val Pro Trp Cys Lys Lys Ser	
105 110 115	
gat gta ata tca agg aga tct gga tac tgc aaa aca cga tta gaa att	438
Asp Val Ile Ser Arg Arg Ser Gly Tyr Cys Lys Thr Arg Leu Glu Ile	
120 125 130	
ggg ttt cca ccc gta ttg gag cgc tat acg tca gta gta acc ttg gtg	486
Gly Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser Val Val Thr Leu Val	
135 140 145	
aaa cca cat ttg gta aag gca tcc tgt gca gat ggg aag ctc ttt aat	534
Lys Pro His Leu Val Lys Ala Ser Cys Ala Asp Gly Lys Leu Phe Asn	
150 155 160 165	
cac tta gag act gtt tgg cgt ttt agc cca ggt ctt cct ggc tac cca	582
His Leu Glu Thr Val Trp Arg Phe Ser Pro Gly Leu Pro Gly Tyr Pro	
170 175 180	
aga act tgt act ttg gat ttt tca att tct ttt gaa ttt cga tca ctt	630
Arg Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu	
185 190 195	
ctg cac tct cag ctt gcc aca ttg ttt ttt gat gaa gtt gtg aag cag	678
Leu His Ser Gln Leu Ala Thr Leu Phe Phe Asp Glu Val Val Lys Gln	
200 205 210	
atg gta gct gct ttt gaa aga aga gca tgt aaa ctg tat ggt cca gaa	726
Met Val Ala Ala Phe Glu Arg Arg Ala Cys Lys Leu Tyr Gly Pro Glu	
215 220 225	
aca agt ata cct cgg gaa tta atg ctt cat gaa gtt cat cac aca taa	774
Thr Ser Ile Pro Arg Glu Leu Met Leu His Glu Val His His Thr	
230 235 240	
gagaaaagga aatgggtgcc tacttgtaac tagtttattc acttttagga agtgctttca 834	

tcatttttgct ytcagaaggc agaaagcatt tgtcaaacac agctttgata taaacctgta 894  
 ctttgcactt ggaatatgga accacatgta catagaattc aatcaagtgt aattcagaat 954  
 aatgtgtata ttagcatatt tacagtaatg ggatgtcatc gctattgtta gaatactgac 1014  
 atcacttttc tgagcagaaa ttgaaactgt aaatttaacc ttttaattat cacctcacct 1074  
 gaaaagggttg gttgagatac tcacgcagca tgtattatat taaccatgtc atgtttaagt 1134  
 tattaaattc agattattta taacttatta tcttagggcc tgcctcatgt cttctagggt 1194  
 atttgagtaa tcatcctata tttaaagtta aaactttgac ttaaaaaaca ctgttaatga 1254  
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 gtactttgac tactatttca gtaatgttga ttgtgtgtca agttttgtct acagcagtgg 1494  
 gcaatagatg aaggaagtcg gttgatatgt ctccaacacc atgcattctg attttctatt 1554  
 tattgtgtat actcactttc aataatgtat ttccaactga tatttttgta aacaaatcag 1614  
 tgtaaggact gaagtggtaa cttaataaag ttaatttggt taaaaaataa aaaaaaaaaa 1674

<210> 19

<211> 244

<212> PRT

<213> Sus sp.

<400> 19

Met	Phe	Val	Ala	Ala	Arg	Thr	Gly	Gln	Arg	Thr	Leu	Arg	Lys	Val	Val
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Ser	Gly	Cys	Arg	Pro	Lys	Ser	Ala	Thr	Ala	Thr	Gly	Val	Pro	Ala	Pro
			20					25					30		

Ala	Gln	Gly	Pro	Pro	Arg	Asn	Ile	Arg	Tyr	Leu	Ala	Ser	Cys	Gly	Ile
		35					40					45			

Leu	Met	Asn	Arg	Thr	Leu	Pro	Leu	His	Ser	Ser	Phe	Leu	Pro	Lys	Glu
	50					55					60				

Met	Tyr	Ala	Arg	Thr	Phe	Phe	Arg	Ile	Ala	Ala	Pro	Leu	Ile	Asn	Lys
	65				70					75					80

Arg	Lys	Glu	Tyr	Ser	Glu	Arg	Arg	Ile	Ile	Gly	Tyr	Ser	Met	Gln	Glu
				85						90				95	

Met	Tyr	Asp	Val	Val	Ser	Gly	Met	Glu	Asp	Tyr	Lys	His	Phe	Val	Pro
			100					105					110		

Trp	Cys	Lys	Lys	Ser	Asp	Val	Ile	Ser	Arg	Arg	Ser	Gly	Tyr	Cys	Lys
		115					120					125			

Thr Arg Leu Glu Ile Gly Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser  
 130 135 140  
 Val Val Thr Leu Val Lys Pro His Leu Val Lys Ala Ser Cys Ala Asp  
 145 150 155 160  
 Gly Lys Leu Phe Asn His Leu Glu Thr Val Trp Arg Phe Ser Pro Gly  
 165 170 175  
 Leu Pro Gly Tyr Pro Arg Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe  
 180 185 190  
 Glu Phe Arg Ser Leu Leu His Ser Gln Leu Ala Thr Leu Phe Phe Asp  
 195 200 205  
 Glu Val Val Lys Gln Met Val Ala Ala Phe Glu Arg Arg Ala Cys Lys  
 210 215 220  
 Leu Tyr Gly Pro Glu Thr Ser Ile Pro Arg Glu Leu Met Leu His Glu  
 225 230 235 240  
 Val His His Thr

<210> 20  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

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 cgcgtggtga atgatctgta

20

<210> 21  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 21  
 ctccatgatc aggtcctcca g

21

<210> 22  
 <211> 607  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Partial  
cDNA sequence of NSE2 from swine

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(192)

&lt;400&gt; 22

gag	gac	ctg	atc	atg	gag	aaa	cgg	cgc	aac	gac	cag	ata	ggg	cgc	gcc	48
Glu	Asp	Leu	Ile	Met	Glu	Lys	Arg	Arg	Asn	Asp	Gln	Ile	Gly	Arg	Ala	
1				5				10					15			

gcg	gtg	cta	cag	gag	ctg	gcc	acg	cac	ctg	cac	ccc	gcg	gag	ccg	gac	96
Ala	Val	Leu	Gln	Glu	Leu	Ala	Thr	His	Leu	His	Pro	Ala	Glu	Pro	Asp	
		20					25					30				

gag	ggc	gac	agc	gac	gcc	gcg	cgg	act	acg	ccg	cct	ccc	ggg	cgc	tcc	144
Glu	Gly	Asp	Ser	Asp	Ala	Ala	Arg	Thr	Thr	Pro	Pro	Pro	Gly	Arg	Ser	
		35					40					45				

cag	gcg	ccg	ggc	caa	gag	gag	gag	gac	cga	gag	gcg	gtg	gtg	cac	tga	192
Gln	Ala	Pro	Gly	Gln	Glu	Glu	Glu	Asp	Arg	Glu	Ala	Val	Val	His		
		50					55					60				

caggcgagct	gagtgcggag	ctgcgtgagg	gagcctttgc	agcagccgct	gccccctccc	252
------------	------------	------------	------------	------------	------------	-----

ttctctccct	ccctcctcca	ccatcttctg	ggccccaaact	gggctcctgg	gccatttgga	312
------------	------------	------------	-------------	------------	------------	-----

aaacggagag	ttggcgaaaa	gcgctgccag	ctgtggcttg	agtttgttat	cttggaacga	372
------------	------------	------------	------------	------------	------------	-----

ggaggaagag	ggagcagctt	ccatggaccc	ctgatcacta	cttgaggaga	attttctctgt	432
------------	------------	------------	------------	------------	-------------	-----

ggattcaact	gactagctat	tgtgatgtaa	gcagtttgag	gtgactggcc	cagcaggagt	492
------------	------------	------------	------------	------------	------------	-----

gagaagaatt	tatcttcagc	ataaacttca	ttattctaca	gtgtttcttc	atttgccctga	552
------------	------------	------------	------------	------------	-------------	-----

gaggtaagga	tgctatgtag	acagaaacaa	aggaagaaaa	aaaaaaaaaa	aaaaa	607
------------	------------	------------	------------	------------	-------	-----

&lt;210&gt; 23

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Partial  
amino acid sequence of NSE2 from swine

&lt;400&gt; 23

Glu	Asp	Leu	Ile	Met	Glu	Lys	Arg	Arg	Asn	Asp	Gln	Ile	Gly	Arg	Ala
1				5					10				15		

Ala	Val	Leu	Gln	Glu	Leu	Ala	Thr	His	Leu	His	Pro	Ala	Glu	Pro	Asp
		20					25					30			

Glu	Gly	Asp	Ser	Asp	Ala	Ala	Arg	Thr	Thr	Pro	Pro	Pro	Gly	Arg	Ser
		35					40					45			

Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His  
 50 55 60

<210> 24  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 24  
 cgagaccctg tgggtggctta ttac 24

<210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 25  
 ctggtgtatt agctggagcg tgtg 24

<210> 26  
 <211> 586  
 <212> DNA  
 <213> Sus sp.

<220>  
 <221> CDS  
 <222> (1)..(585)

<400> 26  
 cga gac cct gtg gtg gct tat tac tgt cgt tta tat gca atg caa act 48  
 Arg Asp Pro Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr  
 1 5 10 15

gga atg aag att gat agt aaa act cct gaa tgt cgt aaa ttt tta tca 96  
 Gly Met Lys Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser  
 20 25 30

aag ctg atg gat cag tta gaa gct ctt aag aaa cag ttg ggt gac aat 144  
 Lys Leu Met Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn  
 35 40 45

gaa gct gtt act caa gaa ata gtt ggt tct gcc cac ttg gag aat tat 192  
 Glu Ala Val Thr Gln Glu Ile Val Gly Ser Ala His Leu Glu Asn Tyr  
 50 55 60

gct ttg aaa atg ttt tta tat gca gat aat gaa gat cgg gct ggg cga	240
Ala Leu Lys Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg	
65 70 75 80	
ttt cat aaa aac atg atc aag tcc ttc tat act gca agt ctt tta ata	288
Phe His Lys Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile	
85 90 95	
gat gtc ata aca gtg ttt gga gaa ctc act gat gaa aat gtg aaa cac	336
Asp Val Ile Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His	
100 105 110	
aga aag tat gca agg tgg aag gca aca tat att cat aat tgt tta aag	384
Arg Lys Tyr Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys	
115 120 125	
aat gga ggg act cct caa gca ggt cct gtg ggc att gaa gaa gat aat	432
Asn Gly Gly Thr Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn	
130 135 140	
gac ata gaa gaa aat gaa gat gct gga gca acc tct ctg ccc act cag	480
Asp Ile Glu Glu Asn Glu Asp Ala Gly Ala Thr Ser Leu Pro Thr Gln	
145 150 155 160	
cca cct cag cca tca tct tcc act tat gac cca ggc aac atg cca tcg	528
Pro Pro Gln Pro Ser Ser Ser Thr Tyr Asp Pro Gly Asn Met Pro Ser	
165 170 175	
agc agc tat act gga ata cag att cct ccc ggt gca cac gct cca gct	576
Ser Ser Tyr Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala	
180 185 190	
aat aca cca g	586
Asn Thr Pro	
195	

<210> 27  
 <211> 195  
 <212> PRT  
 <213> Sus sp.

<400> 27	
Arg Asp Pro Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr	
1 5 10 15	
Gly Met Lys Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser	
20 25 30	
Lys Leu Met Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn	
35 40 45	
Glu Ala Val Thr Gln Glu Ile Val Gly Ser Ala His Leu Glu Asn Tyr	
50 55 60	
Ala Leu Lys Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg	
65 70 75 80	

Phe His Lys Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile  
                     85                    90                    95  
 Asp Val Ile Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His  
                     100                    105                    110  
 Arg Lys Tyr Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys  
                     115                    120                    125  
 Asn Gly Gly Thr Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Asp Asn  
                     130                    135                    140  
 Asp Ile Glu Glu Asn Glu Asp Ala Gly Ala Thr Ser Leu Pro Thr Gln  
                     145                    150                    155                    160  
 Pro Pro Gln Pro Ser Ser Ser Thr Tyr Asp Pro Gly Asn Met Pro Ser  
                     165                    170                    175  
 Ser Ser Tyr Thr Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala  
                     180                    185                    190  
 Asn Thr Pro  
                     195

<210> 28  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           primer

<400> 28  
 aaaaggcccc cagggttacg

20

<210> 29  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
           primer

<400> 29  
 ggagtgggca gcaggtgagc

20

<210> 30  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

&lt;400&gt; 30

ttaacctgca cagcgacaag t

21

&lt;210&gt; 31

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

&lt;400&gt; 31

ttgctgaaga tctcacgctt c

21

&lt;210&gt; 32

&lt;211&gt; 1194

&lt;212&gt; DNA

&lt;213&gt; Sus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(741)

&lt;400&gt; 32

acg	gac	gag	gag	ctc	cgc	agg	cgc	cag	ctg	act	tgc	acc	gag	gag	atg	48
Thr	Asp	Glu	Glu	Leu	Arg	Arg	Arg	Gln	Leu	Thr	Cys	Thr	Glu	Glu	Met	
1				5					10					15		

gcc	cag	cga	ggg	ctg	cgc	cct	gcc	ctt	gac	ccc	tgg	gag	ccg	aag	gcg	96
Ala	Gln	Arg	Gly	Leu	Pro	Pro	Ala	Leu	Asp	Pro	Trp	Glu	Pro	Lys	Ala	
			20					25					30			

gac	tgg	gcg	ccc	gca	ggc	agc	ctc	agc	ggc	gag	gcc	ggc	cag	aag	gat	144
Asp	Trp	Ala	Pro	Ala	Gly	Ser	Leu	Ser	Gly	Glu	Ala	Gly	Gln	Lys	Asp	
		35					40					45				

gtc	aac	ggg	ccc	ctg	agg	gag	ctg	cgc	cca	agg	ctc	tgc	cac	ctg	cga	192
Val	Asn	Gly	Pro	Leu	Arg	Glu	Leu	Arg	Pro	Arg	Leu	Cys	His	Leu	Arg	
	50					55					60					

aaa	ggc	ccc	cag	ggc	tac	ggg	ttt	aac	ctg	cac	agc	gac	aag	tcc	cgg	240
Lys	Gly	Pro	Gln	Gly	Tyr	Gly	Phe	Asn	Leu	His	Ser	Asp	Lys	Ser	Arg	
65					70					75					80	

cct	gga	cag	tac	atc	cgc	tcc	gtg	gac	cca	ggc	tca	cct	gct	gcc	cac	288
Pro	Gly	Gln	Tyr	Ile	Arg	Ser	Val	Asp	Pro	Gly	Ser	Pro	Ala	Ala	His	
				85					90					95		

tcc	ggc	ctc	cga	gcc	cag	gac	cga	ctc	ata	gag	gtg	aac	ggg	cag	aat	336
Ser	Gly	Leu	Arg	Ala	Gln	Asp	Arg	Leu	Ile	Glu	Val	Asn	Gly	Gln	Asn	
			100					105						110		

gtg gag ggg ctg cgg cac gcg gag gtg gtt gcc tgc atc aag gcg cgg 384  
 Val Glu Gly Leu Arg His Ala Glu Val Val Ala Cys Ile Lys Ala Arg  
 115 120 125

gag gac gag gcc cgg ctg ctg gtg gtg gac ccc gag acg gat gtg tac 432  
 Glu Asp Glu Ala Arg Leu Leu Val Val Asp Pro Glu Thr Asp Val Tyr  
 130 135 140

ttc aag cgg ctg cgg gtc aca ccc acc cag gag cac atg gaa ggt cca 480  
 Phe Lys Arg Leu Arg Val Thr Pro Thr Gln Glu His Met Glu Gly Pro  
 145 150 155 160

ctg tca tca cct gtc acc aat ggg acc agc tca gcc cag ctc aat ggt 528  
 Leu Ser Ser Pro Val Thr Asn Gly Thr Ser Ser Ala Gln Leu Asn Gly  
 165 170 175

ggc tcc gtg tgc tcg tcc cga agt gac ctg ccc ggc tta gac aag gac 576  
 Gly Ser Val Cys Ser Ser Arg Ser Asp Leu Pro Gly Leu Asp Lys Asp  
 180 185 190

act gag gac agc agc acc tgg aag cgt gac cct ttc cag gag agt ggc 624  
 Thr Glu Asp Ser Ser Thr Trp Lys Arg Asp Pro Phe Gln Glu Ser Gly  
 195 200 205

ctc cac ctg agc ccc acg gcg gct ggg gcc aag gag aag gcg agg gcc 672  
 Leu His Leu Ser Pro Thr Ala Ala Gly Ala Lys Glu Lys Ala Arg Ala  
 210 215 220

acc agg gtc aac aag cgg gcg cca cag atg gac tgg aac cgg aag cgt 720  
 Thr Arg Val Asn Lys Arg Ala Pro Gln Met Asp Trp Asn Arg Lys Arg  
 225 230 235 240

gag atc ttc agc aac ttc tga gacccccac cctccgccgc agccgccgcc 771  
 Glu Ile Phe Ser Asn Phe  
 245

tgggtccccag ccgggcctcc tctgggcatg gaccttgggc cttgcccaga gcgccccgag 831  
 cctcagtgga ctgcagcggg ggcaccttcg ctgcgtaagc cgtggtggtc ccaccacccc 891  
 ccatgaacca gcccgtgccc cagtgcgccc ccgtcctgcc cccttcccac ggggtgctgg 951  
 ggagcgggca gaggaagccc ctgagacggg agggacagag acaccagag aggtgggctg 1011  
 gggagggggag gttgggggtga cccgccaggc cgggcccttg ctgctctgcc tgggectgct 1071  
 gacttaaagg aatttgtgtt ttggcttttt ttccaacacg agctctggct ccacacatgt 1131  
 ttccacttaa taccagagcc cccaccccca tcccctcagg acgtgctctc taaataattg 1191  
 caa 1194

&lt;210&gt; 33

&lt;211&gt; 246

&lt;212&gt; PRT

&lt;213&gt; Sus sp.

&lt;400&gt; 33

Thr Asp Glu Glu Leu Arg Arg Arg Gln Leu Thr Cys Thr Glu Glu Met  
 1 5 10 15  
 Ala Gln Arg Gly Leu Pro Pro Ala Leu Asp Pro Trp Glu Pro Lys Ala  
 20 25 30  
 Asp Trp Ala Pro Ala Gly Ser Leu Ser Gly Glu Ala Gly Gln Lys Asp  
 35 40 45  
 Val Asn Gly Pro Leu Arg Glu Leu Arg Pro Arg Leu Cys His Leu Arg  
 50 55 60  
 Lys Gly Pro Gln Gly Tyr Gly Phe Asn Leu His Ser Asp Lys Ser Arg  
 65 70 75 80  
 Pro Gly Gln Tyr Ile Arg Ser Val Asp Pro Gly Ser Pro Ala Ala His  
 85 90 95  
 Ser Gly Leu Arg Ala Gln Asp Arg Leu Ile Glu Val Asn Gly Gln Asn  
 100 105 110  
 Val Glu Gly Leu Arg His Ala Glu Val Val Ala Cys Ile Lys Ala Arg  
 115 120 125  
 Glu Asp Glu Ala Arg Leu Leu Val Val Asp Pro Glu Thr Asp Val Tyr  
 130 135 140  
 Phe Lys Arg Leu Arg Val Thr Pro Thr Gln Glu His Met Glu Gly Pro  
 145 150 155 160  
 Leu Ser Ser Pro Val Thr Asn Gly Thr Ser Ser Ala Gln Leu Asn Gly  
 165 170 175  
 Gly Ser Val Cys Ser Ser Arg Ser Asp Leu Pro Gly Leu Asp Lys Asp  
 180 185 190  
 Thr Glu Asp Ser Ser Thr Trp Lys Arg Asp Pro Phe Gln Glu Ser Gly  
 195 200 205  
 Leu His Leu Ser Pro Thr Ala Ala Gly Ala Lys Glu Lys Ala Arg Ala  
 210 215 220  
 Thr Arg Val Asn Lys Arg Ala Pro Gln Met Asp Trp Asn Arg Lys Arg  
 225 230 235 240  
 Glu Ile Phe Ser Asn Phe  
 245

&lt;210&gt; 34

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Sus sp.

&lt;400&gt; 34

Glu Asp Leu Ile Met Glu Lys Arg Arg Asn Asp Gln Ile Gly Arg Ala  
 1 5 10 15

Ala Val Leu Gln Glu Leu Ala Thr His Leu His Pro Ala Glu Pro Asp  
 20 25 30

Glu Gly Asp Ser Asp Ala Ala Arg Thr Thr Pro Pro Pro Gly Arg Ser  
 35 40 45

Gln Ala Pro Gly Gln Glu Glu Glu Asp Arg Glu Ala Val Val His  
 50 55 60

&lt;210&gt; 35

&lt;211&gt; 367

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 clone S064 from BMEC from swine brain

&lt;400&gt; 35

acaataccag ggggtcccca gagagatcct gttcataatt ttgtcctttt taacaccatt 60  
 tcatttgatc aagctgatta gctaagatct tgttacagca tttgcagaaa gcctgaagct 120  
 tgatggataa caacagtgtt aaaccttaag aaatgacaag tataaatata gacacttcaa 180  
 tgtagtttta cattctgagg caagaaatat attatacagg gcctgctgtt tcctctttta 240  
 tgctctaaaa gcaccaatth atgttaaaga tggcaatgtg taattataat cattataatc 300  
 tgattagacc aaacacagga gcaaagctgt aattgctttt agtttttgtt tttttaacat 360  
 gctctgt 367

&lt;210&gt; 36

&lt;211&gt; 3071

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 clone S064.3 from BMEC from swine brain

&lt;220&gt;

&lt;221&gt; modified\_base

&lt;222&gt; (1443)..(1445)

&lt;223&gt; a, c, g, t, unknown, or other

&lt;400&gt; 36

sctwtggcgg ggwatctcwa ggacaaatww waatggaatw atctctggct ggcactcatt 60  
 taattcttaa ctatgtaaaa caacatgagt agaaaaaat ttagtggtat tatgcctaga 120  
 atagataggt gaattccatt gatgtttatc tttgaagacc agctttatgc gtgaactttt 180  
 catctgwgcc tttggatcca aaacatttca tgtccagttc agttctaaag gttcttttat 240  
 attttgtcag ggtagtctct ttgagataca gcatgatgac ttgaatctag cagaatattg 300  
 tgctggctac ctaaaagaagt gggttcaaat cttaatttgg ccattacctt ttgaccttag 360  
 acagttacta ctgtttatgg tcttccttct gtttttcca tgcagaggaa cttaaacaac 420  
 ttatagagtg ccaacatgtc tcttggtttt aaaatcgtga atctattaaa atcccgaatc 480  
 tactaaaaa ctattaaaaa ctggaaaaaa aattcaacta gggaaagaca tgtaatatga 540  
 aatttatatt tacctatcat ttgattccca ctttattatc ytttcattta gtatatgaat 600

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acaatccaat aagaaaatga aggtcaacta ctgccactcc acttaaattg aactaatagt 660
taatgaagtg caaaagagaa aataagccat attgctaaga agatgatata ttaagctgct 720
gataaaatac cagtgtgtgt tgaaaatact cttttagaag ataccttgct tattttcctg 780
gcttttatta attggatgga aatgggttagt ttgatcagag tttattggct ctagaggctg 840
cccccattg tagctctgtt tgactttcca gtattgaaag aatactggaa atgtcaatat 900
tttacaaatg tctgtacaaa tctgaaagta gtttatatcc atgggttagtt ttttcagtaa 960
cgttccatcc ttattcattt agcattactg taaagccagg ttcccaagaa gtattttcta 1020
agagttccaa gtaaccacag ctacatagag aaagccaata aaaacaaaac tttttagcta 1080
cttctctgta aatttaaagt agaaaaaaac cagacctaaa gtcagctttr aatgtatgtg 1140
gtctagttaa atgtttggga aatgtttatt tggagggtta gaggcatacc gaagcaggag 1200
tcaaaacaaa gttgggtgga aagattaaca tgaagtaaaa aaatcttcag tagaaaatag 1260
aaagtttgaa tgaaaacaat gagttgtccc cattcaaggc acttaaaatw actagaaaat 1320
tctgtctttt actgtaattg gatggcctat attatttcta atgtggccaa aggactaaag 1380
accaatcagg tttctagaat tggggagcgt agtcacatag aggcattttt tgcatttttt 1440
aannnaccag taatcttcct tttcccctta gaaakggaga aataaaatgt tctgtacata 1500
tcttttggaa tagaaagcaa aattctagaa gaatggaaat atcctcttac accaacttgt 1560
agttttaatt gaaaaattac ctcatTTTTt agtcacatag gtgctttgct cgagtttgtg 1620
gaatgggtcca ccattcccatt aaaacccgct tcaccaagc tgtatttcaa atatgaaaa 1680
ttcacagcta agggatagca gtccttggag gttttgtttt ccttccactg cgcttaccac 1740
cagcagagct aataacgtga tgtaccaggt tgacatactg cttcattaaa gcacatgggc 1800
aagtgtttag tcaatatTTa attagtttaa ttaaaatcaa ataagggaaa ggaaaaaccc 1860
ttaagtttga ttgagttaca ttatactgtg aatatatttc catctgtgtt gataagacat 1920
caaagtacta tcagttgata ttgattatac ataatttatt tgcattttct ggccctattc 1980
atgagaggct ataattcatt taattcttaca ttttccttca ggaaattcag ggactctaca 2040
gcccctattt tgttctcttg gagtaaaatg ttcagtgtag tttatgaaaa cttttcattt 2100
tggtttttaa aaaggcttag ctgctagttc attaaaagtg tgaaataaaa tgatggttat 2160
gatttttcca attaatgtta taaattttas cstrtycrtc yrwkgtagag agcatgttaa 2220
aaaaacaaaa actaaaagca attacagctt tgctcctgtg tttgggtctaa tcagattata 2280
atgattataa ttacacattg ccatcttaac ataaaattgg gcttttagag cattaaagag 2340
gaaacagcag gccctgtata atatatTTct tgccctcagaa tgtaaaacta cattgaagtg 2400
tctgtattta tacttgtcat ttcttaagggt ttaaaaactg tggtatccat caagcttcag 2460
gctttctgca aatgctgtaa caagatctta gctaatacagc ttgrtcaaat gaaatgggtg 2520
taaaaaggac aaaattatga acaggatctc tctgggggac ccctgggtatt gtacmkrms 2580
ggsggaacy gtctykmag ccacaaactg tgcgtcataa tcccacccaa acaactgaca 2640
tgtgtgtwat tggttcaata cataagcatt aataaaatta aaggaacaaa ttacttaaag 2700
cagtcacatc atcacttcct caaagtgggt yaaagcatgt tcttctaaat ggtggagttg 2760
tttaaagaca tgttttaaat tttgatagct ttactactgt cataaaatgc ttctatatgt 2820
taagtttagg ttgctgggtac tcatgatttt ttacttctgc aattatgctg taatgagttg 2880
cttgcagccc tacttaccce agtgaaagga tgctgtttgc tctggaatgt tcatctttta 2940
gacaggtttk sgctcatttg caatcatggt gcaatacagt gtaacattca tttgttttca 3000
gtcaatagtt ttatttttTg cmcaataaat aattactttt ccaaaaaaaaa aaaaaaaaaa 3060
aaaaaaaaa a 3071

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<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 37

taatgcaggg aaaaccacca ttct

<210> 38  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 38  
aaccaagaga catgttgga ct . 22

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 39  
atagcattga caggaacga ct 22

<210> 40  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 40  
ctgctagatt caagtcacca tgc 23

<210> 41  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 41  
ctcgtgatgg ggctgatctt c 21

<210> 42  
<211> 22  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

&lt;400&gt; 42

atctcacacc aatccgggag gt

22

&lt;210&gt; 43

&lt;211&gt; 540

&lt;212&gt; DNA

&lt;213&gt; Sus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (537)

&lt;400&gt; 43

atg ggg ctg atc ttc gct aaa ctg tgg agc ctc ttc tgt aac caa gag	48
Met Gly Leu Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu	
1 5 10 15	
cac aaa gta att ata gtg gga ctg gat aac gca ggg aag acc act att	96
His Lys Val Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile	
20 25 30	
ctt tat cag ttc tta atg aat gaa gtg gtt cat aca tct cca act ata	144
Leu Tyr Gln Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile	
35 40 45	
gga agc aat gtt gaa gaa ata gtt gtg aag aac act cat ttt ctc atg	192
Gly Ser Asn Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met	
50 55 60	
tgg gat att ggt ggt caa gag tca ctg cgg tca tcc tgg aac acg tat	240
Trp Asp Ile Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr	
65 70 75 80	
tat tca aac aca gag ttc atc att ctt gtg gtt gat agc att gac agg	288
Tyr Ser Asn Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg	
85 90 95	
gaa cga cta gct att acg aaa gaa gaa tta tac aga atg ttg gct cat	336
Glu Arg Leu Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His	
100 105 110	
gag gat tta cgg aag gct gca gtc ctt atc ttt gcc aat aaa cag gat	384
Glu Asp Leu Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp	
115 120 125	
atg aaa ggg tgc atg aca gca gct gaa atc tcc aaa tac ctc acc ctc	432
Met Lys Gly Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu	
130 135 140	
agt tca att aag gat cat ccg tgg cat att cag tcc tgc tgt gct tta	480
Ser Ser Ile Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu	
145 150 155 160	

aca gga gaa ggg tta tgc caa ggt cta gag tgg atg acc tcc cgg att 528  
 Thr Gly Glu Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile  
                   165                                  170                                  175

ggt gtg aga taa 540  
 Gly Val Arg

<210> 44  
 <211> 179  
 <212> PRT  
 <213> Sus sp.

<400> 44  
 Met Gly Leu Ile Phe Ala Lys Leu Trp Ser Leu Phe Cys Asn Gln Glu  
   1                                  5                                  10                                  15  
 His Lys Val Ile Ile Val Gly Leu Asp Asn Ala Gly Lys Thr Thr Ile  
                   20                                  25                                  30  
 Leu Tyr Gln Phe Leu Met Asn Glu Val Val His Thr Ser Pro Thr Ile  
                   35                                  40                                  45  
 Gly Ser Asn Val Glu Glu Ile Val Val Lys Asn Thr His Phe Leu Met  
                   50                                  55                                  60  
 Trp Asp Ile Gly Gly Gln Glu Ser Leu Arg Ser Ser Trp Asn Thr Tyr  
                   65                                  70                                  75                                  80  
 Tyr Ser Asn Thr Glu Phe Ile Ile Leu Val Val Asp Ser Ile Asp Arg  
                   85                                  90                                  95  
 Glu Arg Leu Ala Ile Thr Lys Glu Glu Leu Tyr Arg Met Leu Ala His  
                   100                                  105                                  110  
 Glu Asp Leu Arg Lys Ala Ala Val Leu Ile Phe Ala Asn Lys Gln Asp  
                   115                                  120                                  125  
 Met Lys Gly Cys Met Thr Ala Ala Glu Ile Ser Lys Tyr Leu Thr Leu  
                   130                                  135                                  140  
 Ser Ser Ile Lys Asp His Pro Trp His Ile Gln Ser Cys Cys Ala Leu  
                   145                                  150                                  155                                  160  
 Thr Gly Glu Gly Leu Cys Gln Gly Leu Glu Trp Met Thr Ser Arg Ile  
                   165                                  170                                  175  
 Gly Val Arg

<210> 45  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 45

aagcctgaag cttgatggat aa

22

<210> 46

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 46

caattacagc ttgctcctg tg

22

<210> 47

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 47

atagcattga cagggaaacga ct

22

<210> 48

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 48

gaactgaggg tgaggtatatt gg

22

<210> 49

<211> 332

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic clone 5G9 from BMEC from swine brain

<400> 49

agcggagggc ggcgccatca gcctgctccg caggggtccg ggcgctcttt tcacctggaa 60

```
tattttgaaa acaattgccc tgggtcasat gttgtccttg ygtatatgtg ggacagccat 120
caccagccag tatttggcag aaaaatacaa agtgaatacg cccatgcttc agagctttat 180
caactattgc ttgctgtttc taatttatac aatgatgctg gcatttcagt caggtaataa 240
taacctttta tgcacattga aaaagaaatg gtggaagtat atcctgctcg gactggcaga 300
tgtggaagct aattacctga ttgtcagagc gt 332
```

```
<210> 50
<211> 22
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
primer
```

```
<400> 50
tgtatatgtg ggacagccat ca 22
```

```
<210> 51
<211> 22
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Synthetic
primer
```

```
<400> 51
gtccgagcag gatatacttc ca 22
```

```
<210> 52
<211> 2319
<212> DNA
<213> Sus sp.
```

```
<220>
<221> CDS
<222> (480) .. (1466)
```

```
<220>
<221> modified_base
<222> (662)
<223> g or t
```

```
<400> 52
agtctctctt cagtccacac aagcctcaga aggggtggcct acgggttgga atcgcccctt 60
caatggcacc tcagagacat ctctgcatcg aaaggcaaac cgaacacgtc cttaaggagg 120
agacaccaca gaaacatggt tccaggattc tttaaggacg ggaaagatag ggaagaaaag 180
aaacagaact ataggaaata ccttttacga tagtcaagag ggaggggagac taggtccaag 240
gaggggtcag tcggtcctcc ccagttaaca aaggtcattg cttttcaggt ggcataacct 300
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cgattcacct caggtgctga ttttagataa ggaaccgtaa gaacctgaac cgctcttgg 360  
 gtgtctcctc accccacgca gaagccccac tgccaagacg aagaggaaga gggcatttct 420  
 cctccaactc ctgctccgga ggtgccagga atattttgaa aacaattgcc ctgggtcag 479  
 atg ttg tcc ttg tgt ata tgt ggg aca gcc atc acc agc cag tat ttg 527  
 Met Leu Ser Leu Cys Ile Cys Gly Thr Ala Ile Thr Ser Gln Tyr Leu  
 1 5 10 15  
 gca gaa aaa tac aaa gtg aat acg ccc atg ctt cag agc ttt atc aac 575  
 Ala Glu Lys Tyr Lys Val Asn Thr Pro Met Leu Gln Ser Phe Ile Asn  
 20 25 30  
 tat tgc ttg ctg ttt cta att tat aca atg atg ctg gca ttt cag tca 623  
 Tyr Cys Leu Leu Phe Leu Ile Tyr Thr Met Met Leu Ala Phe Gln Ser  
 35 40 45  
 ggt aat aat aac ctt tta tgc atc ttg aaa aag aaa tgk tgg aag tat 671  
 Gly Asn Asn Asn Leu Leu Cys Ile Leu Lys Lys Lys Xaa Trp Lys Tyr  
 50 55 60  
 atc ctg ctc gga ctg gca gat gtg gaa gct aat tac ctg att gtc aga 719  
 Ile Leu Leu Gly Leu Ala Asp Val Glu Ala Asn Tyr Leu Ile Val Arg  
 65 70 75 80  
 gcg tac cag tac aca act cta acc agt gtc cag ctt ttg gat tgc ttt 767  
 Ala Tyr Gln Tyr Thr Thr Leu Thr Ser Val Gln Leu Leu Asp Cys Phe  
 85 90 95  
 ggg att cct gtg ttg atg gct ctc tcg tgg ttt att ctt tat gca aga 815  
 Gly Ile Pro Val Leu Met Ala Leu Ser Trp Phe Ile Leu Tyr Ala Arg  
 100 105 110  
 tac aga gtg atc cac ttc atc gct gtg gct gtc tgt ctg ttg ggc gta 863  
 Tyr Arg Val Ile His Phe Ile Ala Val Ala Val Cys Leu Leu Gly Val  
 115 120 125  
 gga act atg gtt ggt gca gac ata tta gca ggg aga gaa gac aat tca 911  
 Gly Thr Met Val Gly Ala Asp Ile Leu Ala Gly Arg Glu Asp Asn Ser  
 130 135 140  
 ggt agt gat gtg ctg att ggt gac gtc ttg gtc ctt ctt ggg gcc tcc 959  
 Gly Ser Asp Val Leu Ile Gly Asp Val Leu Val Leu Leu Gly Ala Ser  
 145 150 155 160  
 ctc tat gca gtt tct aat gtg tgt gaa gaa tac atc gtg aag aag ctg 1007  
 Leu Tyr Ala Val Ser Asn Val Cys Glu Glu Tyr Ile Val Lys Lys Leu  
 165 170 175  
 agc cga cag gag ttt tta gga atg gtg ggc ttg ttt gga aca att atc 1055  
 Ser Arg Gln Glu Phe Leu Gly Met Val Gly Leu Phe Gly Thr Ile Ile  
 180 185 190  
 agt ggc ata cag cta ttg att gtg gaa tat aag gat att gcc agc att 1103  
 Ser Gly Ile Gln Leu Leu Ile Val Glu Tyr Lys Asp Ile Ala Ser Ile  
 195 200 205

cac tgg gac tgg aaa att gcc cta ctg ttt gta gca ttt gcc ctc tgt 1151  
 His Trp Asp Trp Lys Ile Ala Leu Leu Phe Val Ala Phe Ala Leu Cys  
 210 215 220

atg ttt tgc ctg tac agc ttc atg cca ctg gtg att aaa gtc act agt 1199  
 Met Phe Cys Leu Tyr Ser Phe Met Pro Leu Val Ile Lys Val Thr Ser  
 225 230 235 240

gcc act tct gtc aac ctg ggc atc ctg aca gct gac ctc tat agt ctt 1247  
 Ala Thr Ser Val Asn Leu Gly Ile Leu Thr Ala Asp Leu Tyr Ser Leu  
 245 250 255

ttc ttt gga ctc ttc ctg ttt ggc tat aag ttc tcg gga ctc tac atc 1295  
 Phe Phe Gly Leu Phe Leu Phe Gly Tyr Lys Phe Ser Gly Leu Tyr Ile  
 260 265 270

ctg tcc ttc gct gtc atc atg gtg ggg ttc att ctg tac tgt tcc acg 1343  
 Leu Ser Phe Ala Val Ile Met Val Gly Phe Ile Leu Tyr Cys Ser Thr  
 275 280 285

ccg acg cgc acg gca gag ccg gct gaa agc agc gtg cca cca cca gtc 1391  
 Pro Thr Arg Thr Ala Glu Pro Ala Glu Ser Ser Val Pro Pro Pro Val  
 290 295 300

acc agc atc ggg atc gac aac ctg ggc ctg aag ctt gag gag aac ctc 1439  
 Thr Ser Ile Gly Ile Asp Asn Leu Gly Leu Lys Leu Glu Glu Asn Leu  
 305 310 315 320

ccg gag acc cac tcc gtg gcc tta tag ctggagaaga aggcacacac 1486  
 Pro Glu Thr His Ser Val Ala Leu  
 325

atgtactgcg gctttctggg aagccgggag ctatcacctg aataaagcag agcctgttgc 1546

ctgctgaggg gacacttggg aaatgatcag atgcagagtg aacactctgg agcactggat 1606

tggctctagt ggtagattt tatgaaggaa tacaaatcaa tgtatcaaag gtagaagtac 1666

caaagtagag cagaagctaa ggcaaggatt gtgtttttgt gtgttttaggg accaatgtgt 1726

attaacgtca gggagacaag gtgtgaggcc cacactgggg tctcagaggc acaagatggg 1786

aaagcaggat ggggtggata ctcaggtgtg aggcagcctc aggcaggggc ctgaaagcag 1846

gctgtccagg taggctgggt ggctcggggag gggaagagca tcccaggatg gtttgggatt 1906

aggtttgctc agttggaggc atctgagttc tgtcctgctg aggcagtgat tgtctcatgg 1966

gctagacgag gtctggtgac tgattgcgta catcaggaag atggaggggtg cagcactgga 2026

gaaatcctga gatacaagtg tagaaccata gaagcagcac agcggatcct tctcccaatt 2086

gttactacac taatcttagc aaataatgtg ccatgagatt tttatgagac ttcttcaaaa 2146

caaagttaac aggaagcatc attatgatat caactaccaa gcagtatgcc mctttacaca 2206

gatgctctat gtaaattttg ggggggtaaa aatataataa aggaatcgag ggtaaattgtt 2266

catattatta aaaatttttg atttcataga aaaaaaaaaa aaaaaaaaaa aaa

2319

<210> 53

<211> 328

<212> PRT

<213> Sus sp.

<220>

<221> MOD\_RES

<222> (61)

<223> Cys or Trp

<400> 53

Met	Leu	Ser	Leu	Cys	Ile	Cys	Gly	Thr	Ala	Ile	Thr	Ser	Gln	Tyr	Leu
1				5					10					15	
Ala	Glu	Lys	Tyr	Lys	Val	Asn	Thr	Pro	Met	Leu	Gln	Ser	Phe	Ile	Asn
			20					25					30		
Tyr	Cys	Leu	Leu	Phe	Leu	Ile	Tyr	Thr	Met	Met	Leu	Ala	Phe	Gln	Ser
	35						40					45			
Gly	Asn	Asn	Asn	Leu	Leu	Cys	Ile	Leu	Lys	Lys	Lys	Xaa	Trp	Lys	Tyr
	50					55					60				
Ile	Leu	Leu	Gly	Leu	Ala	Asp	Val	Glu	Ala	Asn	Tyr	Leu	Ile	Val	Arg
65					70					75					80
Ala	Tyr	Gln	Tyr	Thr	Thr	Leu	Thr	Ser	Val	Gln	Leu	Leu	Asp	Cys	Phe
				85					90					95	
Gly	Ile	Pro	Val	Leu	Met	Ala	Leu	Ser	Trp	Phe	Ile	Leu	Tyr	Ala	Arg
			100					105					110		
Tyr	Arg	Val	Ile	His	Phe	Ile	Ala	Val	Ala	Val	Cys	Leu	Leu	Gly	Val
	115						120					125			
Gly	Thr	Met	Val	Gly	Ala	Asp	Ile	Leu	Ala	Gly	Arg	Glu	Asp	Asn	Ser
	130					135					140				
Gly	Ser	Asp	Val	Leu	Ile	Gly	Asp	Val	Leu	Val	Leu	Leu	Gly	Ala	Ser
145				150					155					160	
Leu	Tyr	Ala	Val	Ser	Asn	Val	Cys	Glu	Glu	Tyr	Ile	Val	Lys	Lys	Leu
				165				170					175		
Ser	Arg	Gln	Glu	Phe	Leu	Gly	Met	Val	Gly	Leu	Phe	Gly	Thr	Ile	Ile
			180					185					190		
Ser	Gly	Ile	Gln	Leu	Leu	Ile	Val	Glu	Tyr	Lys	Asp	Ile	Ala	Ser	Ile
	195						200					205			
His	Trp	Asp	Trp	Lys	Ile	Ala	Leu	Leu	Phe	Val	Ala	Phe	Ala	Leu	Cys
	210					215					220				
Met	Phe	Cys	Leu	Tyr	Ser	Phe	Met	Pro	Leu	Val	Ile	Lys	Val	Thr	Ser
225					230					235				240	

Ala Thr Ser Val Asn Leu Gly Ile Leu Thr Ala Asp Leu Tyr Ser Leu  
 245 250 255

Phe Phe Gly Leu Phe Leu Phe Gly Tyr Lys Phe Ser Gly Leu Tyr Ile  
 260 265 270

Leu Ser Phe Ala Val Ile Met Val Gly Phe Ile Leu Tyr Cys Ser Thr  
 275 280 285

Pro Thr Arg Thr Ala Glu Pro Ala Glu Ser Ser Val Pro Pro Pro Val  
 290 295 300

Thr Ser Ile Gly Ile Asp Asn Leu Gly Leu Lys Leu Glu Glu Asn Leu  
 305 310 315 320

Pro Glu Thr His Ser Val Ala Leu  
 325

<210> 54  
 <211> 407  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 clone 5E7 from BMEC from swine brain

<400> 54  
 acagactgag atttagatgt ttcattggcc gtctgaagag gtgtggcttg tcttttatat 60  
 agagatctac attataaaat actccgtgaa gaaaaacaca ccaaacgaaa gagatttttaa 120  
 gaatttggca cagtttagtcc ctttgtgtaa tctgaactct tctagctgct gaatatcttg 180  
 aagtcattcc tgttcaactga agtcctttctg attgagctgg ttgaataactt tgaaaaatga 240  
 tgcgttctag ctgttgaaat ggatttccca ataggggttc ctgcatatta cctgtatagt 300  
 agctctatgc atatgtttct gtgcatgctc tctaccagtg tgtaagggtg cactgtattt 360  
 taactgttgc acttgtcaac tttcaataaa gcatataaaa tgttggt 407

<210> 55  
 <211> 1905  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: cDNA of TSC-22  
 from BMEC from swine brain

<220>  
 <221> CDS  
 <222> (243)..(677)

<400> 55  
 agtctagagc ctagtggagc ccggctgccg acctgggagc cttctccgca cagcagttgg 60  
 atctgcatct tcccgaatc gccaaagcccc agaagccggg tttctttcaa ttaggggtgc 120

tgttttctgt tcctccctga gccgcataaa gctagaagat ttttatctag ctcaaacaag 180  
 gcctctagaa ttccctcttt tttaattttt ttcctgcgag ggtgtttttt ggctgcaatt 240  
 gc atg aaa tcc caa tgg tgt aga cca gtg gcg atg gat cta gga gtt 287  
 Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val  
 1 5 10 15  
 tac caa ctg aga cat ttt tca att tct ttc ttg tca tcc ttg ctc ggg 335  
 Tyr Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly  
 20 25 30  
 act gaa aac gcc tct gtg aga ctt gac aat agc tct tct ggt gca agt 383  
 Thr Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser  
 35 40 45  
 gtg gta gct att gac aac aaa atc gag caa gct atg gat ctg gtg aaa 431  
 Val Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys  
 50 55 60  
 agc cat ttg atg tat gca gtt aga gag gaa gtg gag gtc ctc aaa gag 479  
 Ser His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu  
 65 70 75  
 caa atc aaa gaa cta ata gag aaa aat tcc cag ctg gag cag gaa aac 527  
 Gln Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn  
 80 85 90 95  
 aat ctg ctg aag aca ctg gcc agt ccg gag cag ctt gcc cag ttc cag 575  
 Asn Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln  
 100 105 110  
 gcc cag ctg cag act ggc tcc ccg ccg gcc acc aca cag ccc cag ggg 623  
 Ala Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly  
 115 120 125  
 acc aca cag ccc ccg gcc cag cca gcg tcc cag ggc tca gga ccg acc 671  
 Thr Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr  
 130 135 140  
 gcg tag cctcctaggc cccccgcag aactggctgc tgcgtgtctga accgactgac 727  
 Ala  
 cgaccgaccg accggagagg atgtgctggg ggaggggggg gtccgcctcc accacggtca 787  
 cccatttcaa tgctcagctg cgaaagagac gtgagactga catatgccat tatctctttt 847  
 ttccagtatt aaacctcat gtgcttttgg cttgaagaag tttcttagtt gggcgactta 907  
 aaggttaacc agagaattag catggatgta ctgggacctc atgcagcggg gcagatccgt 967  
 gagaaatggg ttcatlcatg ctgaggagct gtgtgccttt ccgccccctcc cctgctccgc 1027  
 acccccacct ccacccccac ccctaccctt acccccacct ccgagaggtc gtcgtgcttg 1087  
 ctctctggcgt gctgcgcgca gtccccaagc cgtggagcgc cactggactc tcctctcgct 1147

cctccccac gaggaaccgg aaaggggggt gaaagtcaag accgaagctt catctcacct 1207  
 cggaggaggg gaaacgtagg tcattgtaca cggtgacgac tgtcaccaaa atccataaaa 1267  
 aaacgaaaca aaaaccaag agtactgtgc ctcttcccaa agcaagggat gacgcgggac 1327  
 tattccagag tgactgaagg gtgacaggta gctggcacct cggtatcaa cgtgaaggyg 1387  
 gttttgctca ttgtatattt gtgtatgtag gtgtaactat tttgtacaat agaggactgt 1447  
 aactactatt tagcttgtag agactgagat ttagatgttt cattggccgt ctgaagargt 1507  
 gtggcttgct ttttatatag agatctacat tataaaatac tccgtgaaga aaaacacacc 1567  
 aaacgaaaga gattttaaga atttggcaca gttagtcctt ttgtgtaatc tgaactcttc 1627  
 tagctgctga atatcttgaa gtcatttctt gttcactgaa gtctttctga ttgagctggt 1687  
 tgaatacttt gaaaaaatgat gcgttctagc tgttgaaatg gatttcccaa taggggttcc 1747  
 tgcataattac ctgtatagta gctctatgca tatgtttctg tgcattgctt ctaccaggtt 1807  
 gtaagggtgc actgtatttt aactgttgca cttgtcaact ttcaataaag catataaaat 1867  
 gttggtvmaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1905

<210> 56

<211> 144

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid  
sequence of TSC-22 from BMEC from swine brain

<400> 56

Met	Lys	Ser	Gln	Trp	Cys	Arg	Pro	Val	Ala	Met	Asp	Leu	Gly	Val	Tyr
1				5					10					15	
Gln	Leu	Arg	His	Phe	Ser	Ile	Ser	Phe	Leu	Ser	Ser	Leu	Leu	Gly	Thr
			20					25					30		
Glu	Asn	Ala	Ser	Val	Arg	Leu	Asp	Asn	Ser	Ser	Ser	Gly	Ala	Ser	Val
	35						40					45			
Val	Ala	Ile	Asp	Asn	Lys	Ile	Glu	Gln	Ala	Met	Asp	Leu	Val	Lys	Ser
	50				55					60					
His	Leu	Met	Tyr	Ala	Val	Arg	Glu	Glu	Val	Glu	Val	Leu	Lys	Glu	Gln
65					70				75						80
Ile	Lys	Glu	Leu	Ile	Glu	Lys	Asn	Ser	Gln	Leu	Glu	Gln	Glu	Asn	Asn
			85						90					95	
Leu	Leu	Lys	Thr	Leu	Ala	Ser	Pro	Glu	Gln	Leu	Ala	Gln	Phe	Gln	Ala
			100					105					110		

Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr  
 115 120 125

Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala  
 130 135 140

<210> 57

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 primer

<400> 57

aagaggtgtg gcttgtcttt ta

22

<210> 58

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 primer

<400> 58

tttttcaaag tattcaacca gctc

24

<210> 59

<211> 157

<212> PRT

<213> Homo sapiens

<400> 59

Met Leu Val Leu Leu Ala Gly Ile Phe Val Val His Ile Ala Thr Val  
 1 5 10 15

Ile Met Leu Phe Val Ser Thr Ile Ala Asn Val Trp Leu Val Ser Asn  
 20 25 30

Thr Val Asp Ala Ser Val Gly Leu Trp Lys Asn Cys Thr Asn Ile Ser  
 35 40 45

Cys Ser Asp Ser Leu Ser Tyr Ala Ser Glu Asp Ala Leu Lys Thr Val  
 50 55 60

Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Cys Val Ile Ala Leu Leu  
 65 70 75 80

Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe  
 85 90 95

Leu Ser Gly Ala Thr Thr Leu Val Cys Trp Leu Cys Ile Leu Val Gly  
100 105 110

Val Ser Ile Tyr Thr Ser His Tyr Ala Asn Arg Asp Gly Thr Gln Tyr  
115 120 125

His His Gly Tyr Ser Tyr Ile Leu Gly Trp Ile Cys Phe Cys Phe Ser  
130 135 140

Phe Ile Ile Gly Val Leu Tyr Leu Val Leu Arg Lys Lys  
145 150 155

<210> 60

<211> 160

<212> PRT

<213> Mus sp.

<400> 60

Met Leu Val Leu Leu Ala Gly Leu Phe Val Val His Ile Ala Thr Ala  
1 5 10 15

Ile Met Leu Phe Val Ser Thr Ile Ala Asn Val Trp Met Val Ala Asp  
20 25 30

Tyr Ala Asn Ala Ser Val Gly Leu Trp Lys Asn Cys Thr Gly Gly Asn  
35 40 45

Cys Asp Gly Ser Leu Ser Tyr Gly Asn Glu Asp Ala Ile Lys Ala Val  
50 55 60

Gln Ala Phe Met Ile Leu Ser Ile Ile Phe Ser Ile Ile Ser Leu Val  
65 70 75 80

Val Phe Val Phe Gln Leu Phe Thr Met Glu Lys Gly Asn Arg Phe Phe  
85 90 95

Leu Ser Gly Ser Thr Met Leu Val Cys Trp Leu Cys Ile Leu Val Gly  
100 105 110

Val Ser Ile Tyr Thr His His Tyr Ala His Ser Glu Gly Asn Phe Asn  
115 120 125

Ser Ser Ser His Gln Gly Tyr Cys Phe Ile Leu Thr Trp Ile Cys Phe  
130 135 140

Cys Phe Ser Phe Ile Ile Gly Ile Leu Tyr Met Val Leu Arg Lys Lys  
145 150 155 160

<210> 61

<211> 238

<212> PRT

<213> Homo sapiens

&lt;400&gt; 61

Met Ala Ala Arg Thr Gly His Thr Ala Leu Arg Arg Val Val Ser Gly  
 1 5 10 15

Cys Arg Pro Lys Ser Ala Thr Ala Ala Gly Ala Gln Ala Pro Val Arg  
 20 25 30

Asn Gly Arg Tyr Leu Ala Ser Cys Gly Ile Leu Met Ser Arg Thr Leu  
 35 40 45

Pro Leu His Thr Ser Ile Leu Pro Lys Glu Ile Cys Ala Arg Thr Phe  
 50 55 60

Phe Lys Ile Thr Ala Pro Leu Ile Asn Lys Arg Lys Glu Tyr Ser Glu  
 65 70 75 80

Arg Arg Ile Leu Gly Tyr Ser Met Gln Glu Met Tyr Asp Val Val Ser  
 85 90 95

Gly Val Glu Asp Tyr Lys His Phe Val Pro Trp Cys Lys Lys Ser Asp  
 100 105 110

Val Ile Ser Lys Arg Ser Gly Tyr Cys Lys Thr Arg Leu Glu Ile Gly  
 115 120 125

Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser Val Val Thr Leu Val Lys  
 130 135 140

Pro His Leu Val Lys Ala Ser Cys Thr Asp Gly Arg Leu Phe Asn His  
 145 150 155 160

Leu Glu Thr Ile Trp Arg Phe Ser Pro Gly Leu Pro Gly Tyr Pro Arg  
 165 170 175

Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe Glu Phe Arg Ser Leu Leu  
 180 185 190

His Ser Gln Leu Ala Thr Leu Phe Phe Asp Glu Val Val Lys Gln Met  
 195 200 205

Val Ala Ala Phe Glu Arg Arg Ala Cys Lys Leu Tyr Gly Pro Glu Thr  
 210 215 220

Asn Ile Pro Arg Glu Leu Met Leu His Glu Val His His Thr  
 225 230 235

&lt;210&gt; 62

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 62

Met Ile Met Ala Ala Arg Thr Ser Gln Arg Ala Leu Ala Arg Val Ala  
 1 5 10 15

Ser Gly Cys His Pro Lys Ser Thr Thr Val Thr Glu Ala Pro Ala Arg  
 20 25 30

Gly Ser Ala Arg Asp Val Arg His Leu Ala Ala Cys Gly Val Leu Ile  
                   35                                  40                                  45  
 Asn Arg Thr Leu Pro Pro Cys Ala Ala Val Leu Pro Lys Glu Ile Cys  
                   50                                  55                                  60  
 Ala Arg Thr Phe Phe Arg Ile Ser Ala Pro Leu Val Asn Lys Arg Lys  
                   65                                  70                                  75                                  80  
 Glu Tyr Ser Glu Arg Arg Ile Leu Gly Tyr Ser Met Gln Glu Met Tyr  
                                   85                                  90                                  95  
 Asp Val Val Ser Gly Met Glu Asp Tyr Gln His Phe Val Pro Trp Cys  
                                   100                                  105                                  110  
 Lys Lys Ser Asp Ile Ile Ser Arg Arg Ser Gly Tyr Cys Lys Thr Arg  
                   115                                  120                                  125  
 Leu Glu Val Gly Phe Pro Pro Val Leu Glu Arg Tyr Thr Ser Ile Val  
                   130                                  135                                  140  
 Thr Leu Val Lys Pro His Leu Val Lys Ala Ser Cys Thr Asp Gly Lys  
                   145                                  150                                  155                                  160  
 Leu Phe Asn His Leu Glu Thr Ile Trp Arg Phe Ser Pro Gly Leu Pro  
                                   165                                  170                                  175  
 Gly Tyr Pro Arg Thr Cys Thr Leu Asp Phe Ser Ile Ser Phe Glu Phe  
                                   180                                  185                                  190  
 Arg Ser Leu Leu His Ser Gln Leu Ala Thr Leu Phe Phe Asp Glu Val  
                   195                                  200                                  205  
 Val Lys Gln Met Val Ala Ala Phe Glu Arg Arg Ala Cys Lys Leu Tyr  
                   210                                  215                                  220  
 Gly Pro Glu Thr Asn Ile Pro Arg Glu Leu Met Leu His Glu Ile His  
                   225                                  230                                  235                                  240  
 His Thr

<210> 63  
 <211> 310  
 <212> PRT  
 <213> Homo sapiens

<400> 63  
 Met Gly Asn Gln Val Glu Lys Leu Thr His Leu Ser Tyr Lys Glu Val  
           1                                  5                                  10                                  15  
 Pro Thr Ala Asp Pro Thr Gly Val Asp Arg Asp Asp Gly Pro Arg Ile  
                   20                                  25                                  30  
 Gly Val Ser Tyr Ile Phe Ser Asn Asp Asp Glu Asp Val Glu Pro Gln  
                   35                                  40                                  45

Pro Pro Pro Gln Gly Pro Asp Gly Gly Gly Leu Pro Asp Gly Gly Asp  
 50 55 60  
 Gly Pro Pro Pro Pro Gln Pro Gln Pro Tyr Asp Pro Arg Leu His Glu  
 65 70 75 80  
 Val Glu Cys Ser Val Phe Tyr Arg Asp Glu Cys Ile Tyr Gln Lys Ser  
 85 90 95  
 Phe Ala Pro Gly Ser Ala Ala Leu Ser Thr Tyr Thr Pro Glu Asn Leu  
 100 105 110  
 Leu Asn Lys Cys Lys Pro Gly Asp Leu Val Glu Phe Val Ser Gln Ala  
 115 120 125  
 Gln Tyr Pro His Trp Ala Val Tyr Val Gly Asn Phe Gln Val Val His  
 130 135 140  
 Leu His Arg Leu Glu Val Ile Asn Ser Phe Leu Thr Asp Ala Ser Gln  
 145 150 155 160  
 Gly Arg Arg Gly Arg Val Val Asn Asp Leu Tyr Arg Tyr Lys Pro Leu  
 165 170 175  
 Ser Ser Ser Ala Val Val Arg Asn Ala Leu Ala His Val Gly Ala Lys  
 180 185 190  
 Glu Arg Glu Leu Ser Trp Arg Asn Ser Glu Ser Phe Ala Ala Trp Cys  
 195 200 205  
 Arg Tyr Gly Lys Arg Glu Phe Lys Ile Gly Gly Glu Leu Arg Ile Gly  
 210 215 220  
 Lys Gln Pro Tyr Arg Leu Gln Ile Gln Leu Ser Ala Gln Arg Ser His  
 225 230 235 240  
 Thr Leu Glu Phe Gln Ser Leu Glu Asp Leu Ile Met Glu Lys Arg Arg  
 245 250 255  
 Asn Asp Gln Ile Gly Arg Ala Ala Val Leu Gln Glu Leu Ala Thr His  
 260 265 270  
 Leu His Pro Ala Glu Pro Glu Glu Gly Asp Ser Asn Val Ala Arg Thr  
 275 280 285  
 Thr Pro Pro Pro Gly Arg Pro Pro Ala Pro Ser Ser Glu Glu Glu Asp  
 290 295 300  
 Gly Glu Ala Val Ala His  
 305 310

&lt;210&gt; 64

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

Met 1	Gly	Asn	Gln	Leu	Asp	Arg	Ile	Thr	His	Leu	Asn	Tyr	Ser	Glu	Leu
5									10					15	
Pro	Thr	Gly	Asp	Pro	Ser	Gly	Ile	Glu	Lys	Asp	Glu	Leu	Arg	Val	Gly
20								25					30		
Val	Ala	Tyr	Phe	Phe	Ser	Asp	Asp	Glu	Glu	Asp	Leu	Asp	Glu	Arg	Gly
35							40					45			
Gln	Pro	Asp	Lys	Phe	Gly	Val	Lys	Ala	Pro	Pro	Gly	Cys	Thr	Pro	Cys
50						55					60				
Pro	Glu	Ser	Pro	Ser	Arg	His	Gln	His	His	Leu	Leu	His	Gln	Leu	Val
65					70					75					80
Leu	Asn	Glu	Thr	Gln	Phe	Ser	Ala	Phe	Arg	Gly	Gln	Glu	Cys	Ile	Phe
85									90					95	
Ser	Lys	Val	Ser	Gly	Gly	Pro	Gln	Gly	Ala	Asp	Leu	Ser	Val	Tyr	Ala
100								105					110		
Val	Thr	Ala	Leu	Pro	Ala	Leu	Cys	Glu	Pro	Gly	Asp	Leu	Leu	Glu	Leu
115							120					125			
Leu	Trp	Leu	Gln	Pro	Ala	Pro	Glu	Pro	Pro	Ala	Pro	Ala	Pro	His	Trp
130						135					140				
Ala	Val	Tyr	Val	Gly	Gly	Gly	Gln	Ile	Ile	His	Leu	His	Gln	Gly	Glu
145					150					155					160
Ile	Arg	Gln	Asp	Ser	Leu	Tyr	Glu	Ala	Gly	Ala	Ala	Asn	Val	Gly	Arg
				165					170					175	
Val	Val	Asn	Ser	Trp	Tyr	Arg	Tyr	Arg	Pro	Leu	Val	Ala	Glu	Leu	Val
180								185					190		
Val	Gln	Asn	Ala	Cys	Gly	His	Leu	Gly	Leu	Lys	Ser	Glu	Glu	Ile	Cys
195							200					205			
Trp	Thr	Asn	Ser	Glu	Ser	Phe	Ala	Ala	Trp	Cys	Arg	Phe	Gly	Lys	Arg
210						215					220				
Glu	Phe	Lys	Ala	Gly	Gly	Glu	Val	Pro	Ala	Gly	Thr	Gln	Pro	Pro	Gln
225					230					235					240
Gln	Gln	Tyr	Tyr	Leu	Lys	Val	His	Leu	Gly	Glu	Asn	Lys	Val	His	Thr
				245					250					255	
Ala	Arg	Phe	His	Ser	Leu	Glu	Asp	Leu	Ile	Arg	Glu	Lys	Arg	Arg	Ile
260								265					270		
Asp	Ala	Ser	Gly	Arg	Leu	Arg	Val	Leu	Gln	Glu	Leu	Ala	Asp	Leu	Val
275							280					285			
Asp	Asp	Lys	Glu												
290															

<210> 65  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens

<400> 65

Met	Ala	Ala	Leu	Ala	Pro	Leu	Pro	Pro	Leu	Pro	Ala	Gln	Leu	Lys	Ser	1	5	10	15
Ile	Gln	His	His	Leu	Arg	Thr	Ala	Gln	Glu	His	Asp	Lys	Arg	Asp	Pro	20	25	30	
Val	Val	Ala	Tyr	Tyr	Cys	Arg	Leu	Tyr	Ala	Met	Gln	Thr	Gly	Met	Lys	35	40	45	
Ile	Asp	Ser	Lys	Thr	Pro	Glu	Cys	Arg	Lys	Phe	Leu	Ser	Lys	Leu	Met	50	55	60	
Asp	Gln	Leu	Glu	Ala	Leu	Lys	Lys	Gln	Leu	Gly	Asp	Asn	Glu	Ala	Ile	65	70	75	80
Thr	Gln	Glu	Ile	Val	Gly	Cys	Ala	His	Leu	Glu	Asn	Tyr	Ala	Leu	Lys	85	90	95	
Met	Phe	Leu	Tyr	Ala	Asp	Asn	Glu	Asp	Arg	Ala	Gly	Arg	Phe	His	Lys	100	105	110	
Asn	Met	Ile	Lys	Ser	Phe	Tyr	Thr	Ala	Ser	Leu	Leu	Ile	Asp	Val	Ile	115	120	125	
Thr	Val	Phe	Gly	Glu	Leu	Thr	Asp	Glu	Asn	Val	Lys	His	Arg	Lys	Tyr	130	135	140	
Ala	Arg	Trp	Lys	Ala	Thr	Tyr	Ile	His	Asn	Cys	Leu	Lys	Asn	Gly	Glu	145	150	155	160
Thr	Pro	Gln	Ala	Gly	Pro	Val	Gly	Ile	Glu	Glu	Asp	Asn	Asp	Ile	Glu	165	170	175	
Glu	Asn	Glu	Asp	Ala	Gly	Ala	Ala	Ser	Leu	Pro	Thr	Gln	Pro	Thr	Gln	180	185	190	
Pro	Ser	Ser	Ser	Ser	Thr	Tyr	Asp	Pro	Ser	Asn	Met	Pro	Ser	Gly	Asn	195	200	205	
Tyr	Thr	Gly	Ile	Gln	Ile	Pro	Pro	Gly	Ala	His	Ala	Pro	Ala	Asn	Thr	210	215	220	
Pro	Ala	Glu	Val	Pro	His	Ser	Thr	Gly	Val	Ala	Ser	Asn	Thr	Ile	Gln	225	230	235	240
Pro	Thr	Pro	Gln	Thr	Ile	Pro	Ala	Ile	Asp	Pro	Ala	Leu	Phe	Asn	Thr	245	250	255	
Ile	Ser	Gln	Gly	Asp	Val	Arg	Leu	Thr	Pro	Glu	Asp	Phe	Ala	Arg	Ala	260	265	270	

Gln Lys Tyr Cys Lys Tyr Ala Gly Ser Ala Leu Gln Tyr Glu Asp Val  
 275 280 285

Ser Thr Ala Val Gln Asn Leu Gln Lys Ala Leu Lys Leu Leu Thr Thr  
 290 295 300

Gly Arg Glu  
 305

<210> 66  
 <211> 309  
 <212> PRT  
 <213> Mus sp.

<400> 66  
 Met Ala Ala Leu Ala Pro Leu Pro Pro Leu Pro Ala Gln Phe Lys Ser  
 1 5 10 15

Ile Gln His His Leu Arg Thr Ala Gln Glu His Asp Lys Arg Asp Pro  
 20 25 30

Val Val Ala Tyr Tyr Cys Arg Leu Tyr Ala Met Gln Thr Gly Met Lys  
 35 40 45

Ile Asp Ser Lys Thr Pro Glu Cys Arg Lys Phe Leu Ser Lys Leu Met  
 50 55 60

Asp Gln Leu Glu Ala Leu Lys Lys Gln Leu Gly Asp Asn Glu Ala Val  
 65 70 75 80

Thr Gln Glu Ile Val Gly Cys Ala His Leu Glu Asn Tyr Ala Leu Lys  
 85 90 95

Met Phe Leu Tyr Ala Asp Asn Glu Asp Arg Ala Gly Arg Phe His Lys  
 100 105 110

Asn Met Ile Lys Ser Phe Tyr Thr Ala Ser Leu Leu Ile Asp Val Ile  
 115 120 125

Thr Val Phe Gly Glu Leu Thr Asp Glu Asn Val Lys His Arg Lys Tyr  
 130 135 140

Ala Arg Trp Lys Ala Thr Tyr Ile His Asn Cys Leu Lys Asn Gly Glu  
 145 150 155 160

Thr Pro Gln Ala Gly Pro Val Gly Ile Glu Glu Glu Asn Asp Val Glu  
 165 170 175

Glu Asn Glu Asp Val Gly Ala Thr Ser Leu Pro Thr Gln Pro Pro Gln  
 180 185 190

Pro Ser Ser Ser Ser Ala Tyr Asp Pro Ser Asn Leu Ala Pro Gly Ser  
 195 200 205

Tyr Ser Gly Ile Gln Ile Pro Pro Gly Ala His Ala Pro Ala Asn Thr  
 210 215 220

Pro Ala Glu Val Pro His Ser Thr Gly Val Thr Ser Asn Ala Val Gln  
225 230 235 240

Pro Ser Pro Gln Thr Val Pro Ala Ala Pro Ala Val Asp Pro Asp Leu  
245 250 255

Tyr Thr Ala Ser Gln Gly Asp Ile Arg Leu Thr Pro Glu Asp Phe Ala  
260 265 270

Arg Ala Gln Lys Tyr Cys Lys Tyr Ala Gly Ser Ala Leu Gln Tyr Glu  
275 280 285

Asp Val Gly Thr Ala Val Gln Asn Leu Gln Lys Ala Leu Arg Leu Leu  
290 295 300

Thr Thr Gly Arg Glu  
305

<210> 67

<211> 450

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Ala Pro Glu Pro Leu Arg Pro Arg Leu Cys Arg Leu Val Arg  
1 5 10 15

Gly Glu Gln Gly Tyr Gly Phe His Leu His Gly Glu Lys Gly Arg Arg  
20 25 30

Gly Gln Phe Ile Arg Arg Val Glu Pro Gly Ser Pro Ala Glu Ala Ala  
35 40 45

Ala Leu Ala Gly Asp Arg Leu Val Glu Val Asn Gly Val Asn Val Glu  
50 55 60

Gly Glu Thr His His Gln Val Val Gln Arg Ile Lys Ala Val Glu Gly  
65 70 75 80

Gln Thr Arg Leu Leu Val Val Asp Gln Glu Thr Asp Glu Glu Leu Arg  
85 90 95

Arg Arg Gln Leu Thr Cys Thr Glu Glu Met Ala Gln Arg Gly Leu Pro  
100 105 110

Pro Ala His Asp Pro Trp Glu Pro Lys Pro Asp Trp Ala His Thr Gly  
115 120 125

Ser His Ser Ser Glu Ala Gly Lys Lys Asp Val Ser Gly Pro Leu Arg  
130 135 140

Glu Leu Arg Pro Arg Leu Cys His Leu Arg Lys Gly Pro Gln Gly Tyr  
145 150 155 160

Gly Phe Asn Leu His Ser Asp Lys Ser Arg Pro Gly Gln Tyr Ile Arg  
165 170 175

Ser Val Asp Pro Gly Ser Pro Ala Ala Arg Ser Gly Leu Arg Ala Gln  
 180 185 190  
 Asp Arg Leu Ile Glu Val Asn Gly Gln Asn Val Glu Gly Leu Arg His  
 195 200 205  
 Ala Glu Val Val Ala Ser Ile Lys Ala Arg Glu Asp Glu Ala Arg Leu  
 210 215 220  
 Leu Val Val Asp Pro Glu Thr Asp Glu His Phe Lys Arg Leu Arg Val  
 225 230 235 240  
 Thr Pro Thr Glu Glu His Val Glu Gly Pro Leu Pro Ser Pro Val Thr  
 245 250 255  
 Asn Gly Thr Ser Pro Ala Gln Leu Asn Gly Gly Ser Ala Cys Ser Ser  
 260 265 270  
 Arg Ser Asp Leu Pro Gly Ser Asp Lys Asp Thr Glu Asp Gly Ser Ala  
 275 280 285  
 Trp Lys Gln Asp Pro Phe Gln Glu Ser Gly Leu His Leu Ser Pro Thr  
 290 295 300  
 Ala Ala Glu Ala Arg Arg Arg Leu Glu Pro Cys Glu Ser Thr Ser Ala  
 305 310 315 320  
 Arg His Arg Trp Thr Gly Thr Gly Ser Val Lys Ser Ser Ala Thr Ser  
 325 330 335  
 Glu Pro Leu Pro Ala Cys Leu Gly Thr Leu Gly Pro Leu Pro His Gly  
 340 345 350  
 Pro Trp Ala Ser Ala Cys Pro Glu Leu Pro Gln Pro Gln Trp Thr Gly  
 355 360 365  
 Gly Trp Ser Cys His Cys Pro Glu Ile Ser Pro Ser Pro Gly Glu Pro  
 370 375 380  
 Pro Ser Cys Pro Cys Pro Pro Gly Thr Gly Gly Leu Trp Gln Gln Asp  
 385 390 395 400  
 Arg Gly Arg Glu Thr Gln Arg Cys Glu Arg Glu Ser Glu Thr Glu Thr  
 405 410 415  
 Glu Arg Glu Arg Glu Arg His Arg Glu Arg Gln Arg Glu Ser Glu Arg  
 420 425 430  
 Ala Arg Gly Ser Arg Gly Ala Arg Ala Phe Ala Ala Leu Pro Gly Pro  
 435 440 445  
 Ala Asp  
 450

<210> 68  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Leu Ser Leu Cys Ile Cys Gly Thr Ala Ile Thr Ser Gln Tyr Leu  
   1                  5                  10                  15  
 Ala Glu Arg Tyr Lys Val Asn Thr Pro Met Leu Gln Ser Phe Ile Asn  
                   20                  25                  30  
 Tyr Cys Leu Leu Phe Leu Ile Tyr Thr Val Met Leu Ala Phe Arg Ser  
           35                  40                  45  
 Gly Ser Asp Asn Leu Leu Val Ile Leu Lys Arg Lys Trp Trp Lys Tyr  
   50                  55                  60  
 Ile Leu Leu Gly Leu Ala Asp Val Glu Ala Asn Tyr Val Ile Val Arg  
   65                  70                  75                  80  
 Ala Tyr Gln Tyr Thr Thr Leu Thr Ser Val Gln Leu Leu Asp Cys Phe  
                   85                  90                  95  
 Gly Ile Pro Val Leu Met Ala Leu Ser Trp Phe Ile Leu His Ala Arg  
           100                  105                  110  
 Tyr Arg Val Ile His Phe Ile Ala Val Ala Val Cys Leu Leu Gly Val  
   115                  120                  125  
 Gly Thr Met Val Gly Ala Asp Ile Leu Ala Gly Arg Glu Asp Asn Ser  
   130                  135                  140  
 Gly Ser Asp Val Leu Ile Gly Asp Ile Leu Val Leu Leu Gly Ala Ser  
   145                  150                  155                  160  
 Leu Tyr Ala Ile Ser Asn Val Cys Glu Glu Tyr Ile Val Lys Lys Leu  
           165                  170                  175  
 Ser Arg Gln Glu Phe Leu Gly Met Val Gly Leu Phe Gly Thr Ile Ile  
           180                  185                  190  
 Ser Gly Ile Gln Leu Leu Ile Val Glu Tyr Lys Asp Ile Ala Ser Ile  
   195                  200                  205  
 His Trp Asp Trp Lys Ile Ala Leu Leu Phe Val Ala Phe Ala Leu Cys  
   210                  215                  220  
 Met Phe Cys Leu Tyr Ser Phe Met Pro Leu Val Ile Lys Val Thr Ser  
   225                  230                  235                  240  
 Ala Thr Ser Val Asn Leu Gly Ile Leu Thr Ala Asp Leu Tyr Ser Leu  
           245                  250                  255  
 Phe Val Gly Leu Phe Leu Phe Gly Tyr Lys Phe Ser Gly Leu Tyr Ile  
   260                  265                  270

Leu Ser Phe Thr Val Ile Met Val Gly Phe Ile Leu Tyr Cys Ser Thr  
 275 280 285

Pro Thr Arg Thr Ala Glu Pro Ala Glu Ser Ser Val Pro Pro Val Thr  
 290 295 300

Ser Ile Gly Ile Asp Asn Leu Gly Leu Lys Leu Glu Glu Asn Leu Gln  
 305 310 315 320

Glu Thr His Ser Ala Val Leu  
 325

<210> 69

<211> 328

<212> PRT

<213> Sus sp.

<400> 69

Met Leu Ser Leu Cys Ile Cys Gly Thr Ala Ile Thr Ser Gln Tyr Leu  
 1 5 10 15

Ala Glu Lys Tyr Lys Val Asn Thr Pro Met Leu Gln Ser Phe Ile Asn  
 20 25 30

Tyr Cys Leu Leu Phe Leu Ile Tyr Thr Met Met Leu Ala Phe Gln Ser  
 35 40 45

Gly Asn Asn Asn Leu Leu Cys Ile Leu Lys Lys Lys Trp Trp Lys Tyr  
 50 55 60

Ile Leu Leu Gly Leu Ala Asp Val Glu Ala Asn Tyr Leu Ile Val Arg  
 65 70 75 80

Ala Tyr Gln Tyr Thr Thr Leu Thr Ser Val Gln Leu Leu Asp Cys Phe  
 85 90 95

Gly Ile Pro Val Leu Met Ala Leu Ser Trp Phe Ile Leu Tyr Ala Arg  
 100 105 110

Tyr Arg Val Ile His Phe Ile Ala Val Ala Val Cys Leu Leu Gly Val  
 115 120 125

Gly Thr Met Val Gly Ala Asp Ile Leu Ala Gly Arg Glu Asp Asn Ser  
 130 135 140

Gly Ser Asp Val Leu Ile Gly Asp Val Leu Val Leu Leu Gly Ala Ser  
 145 150 155 160

Leu Tyr Ala Val Ser Asn Val Cys Glu Glu Tyr Ile Val Lys Lys Leu  
 165 170 175

Ser Arg Gln Glu Phe Leu Gly Met Val Gly Leu Phe Gly Thr Ile Ile  
 180 185 190

Ser Gly Ile Gln Leu Leu Ile Val Glu Tyr Lys Asp Ile Ala Ser Ile  
 195 200 205

His Trp Asp Trp Lys Ile Ala Leu Leu Phe Val Ala Phe Ala Leu Cys  
 210 215 220

Met Phe Cys Leu Tyr Ser Phe Met Pro Leu Val Ile Lys Val Thr Ser  
 225 230 235 240

Ala Thr Ser Val Asn Leu Gly Ile Leu Thr Ala Asp Leu Tyr Ser Leu  
 245 250 255

Phe Phe Gly Leu Phe Leu Phe Gly Tyr Lys Phe Ser Gly Leu Tyr Ile  
 260 265 270

Leu Ser Phe Ala Val Ile Met Val Gly Phe Ile Leu Tyr Cys Ser Thr  
 275 280 285

Pro Thr Arg Thr Ala Glu Pro Ala Glu Ser Ser Val Pro Pro Pro Val  
 290 295 300

Thr Ser Ile Gly Ile Asp Asn Leu Gly Leu Lys Leu Glu Glu Asn Leu  
 305 310 315 320

Pro Glu Thr His Ser Val Ala Leu  
 325

<210> 70

<211> 11

<212> PRT

<213> Homo sapiens

<400> 70

Asp Gly Ser Ala Trp Lys Gln Asp Pro Phe Gln  
 1 5 10